

**AMENDMENTS TO THE SPECIFICATION**

Please delete the sequence listing from the published international application and replace with the sequence listing submitted on compact disc enclosed herewith.

In the specification at page 1, after the title and before line 3, please insert the following:

**-- RELATED APPLICATIONS**

This application is a national stage application (under 35 U.S.C. 371) of PCT/EP2004/008683 filed August 3, 2004 which claims benefit of European patent application 03018266.1 filed August 11, 2003.

**SUBMISSION ON COMPACT DISC**

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: two copies of the Sequence Listing (COPY 1 and COPY 2) and a computer readable form copy of the Sequence Listing (CRF COPY), all on compact disc, each containing: file name: Final Sequence list-13477-00002-US, date recorded: February 10, 2006, size: 166 KB. --

In the specification at page 72-73, please replace Table 3A with the following amended Table 3A:

**Table 3A.** Overview of markers used for mapping Rpiblb2

Marker	Ori <sup>1)</sup>	Sequence	SEQ ID NO:	Annealing temp (°C)	Restriction Enzyme <sup>2)</sup>
E46M52	F	TTGTGGTTATCGATGAGAAT	<u>11</u>	56,5	SCAR (b)
	R	GAAACAACAGCAGGATAGTGAG	<u>12</u>		SCAR
E46M52e	F	TTGTGGTTATCGATGAGAAT	<u>13</u>	61	(a,b);MboI (c)
	R	GAAACAACAGCAGGATAGTGAG	<u>14</u>		
E40M58	F	GAATTCAGCACAAATACCAA	<u>15</u>	50	DdeI (a)
	R	TTAACGTTTACTATCACGAG	<u>16</u>		
E40M58e	F	GTAGAAACAGCAGCCTCATAAGC	<u>17</u>	55	SCAR (a)
	R	TTCTGCCTAATTGCCCTGTG	<u>18</u>		
S1E00	F	GGGGTTGGGAAGACAACGACAC	<u>19</u>	50	AFLP
	R	AATTCCAAGATACAGTCAAATAC	<u>20</u>		
41L	F	AGGCAGGATTAACAGTAGAAG	<u>21</u>	58	TaqI (a)
	R	CATGCTTTTAGGAAGAAGCTC	<u>22</u>		
36L	F	TTGAGACAAAGCAGCTCCAC	<u>23</u>	59	ApoI (a,b)
	R	ACGTTTCTCACACCTACAGG	<u>24</u>		
69L	F	TGATGGCACGTTTGATCGTG	<u>25</u>	61	TaqI (a,b);HpaII (c)
	R	TAAGATCCAAACCAGCCACC	<u>26</u>		
69R	F	CCTTATCACACATGTGGCTAC	<u>27</u>	58	RsaI (a,b); ApoI (c)
	R	ATTGAAACGGAGGAAGTACAAC	<u>28</u>		
141R	F	TTCTTCATATGGCAGACCAAC	<u>29</u>	60	RsaI (a,b); DdeI (c)
	R	CTACTCTGCTGACATGCAGG	<u>30</u>		
24L	F	GAGATTCTCAAAGGTGTCTTCC	<u>31</u>	60	SCAR (a,b,c)
	R	AACCTGTGCTTTCCCATTCG	<u>32</u>		
24R	F	CTTTCACAAGCGTCACTTTGG	<u>33</u>	58	SCAR (a,b)
	R	TAAAAAGAATCAACAGGGCAAC	<u>34</u>		
14L	F	ACGACTGCTCAAAGTTGGCC	<u>35</u>	58	SCAR (a,b,c)
	R	CCAAGAAGCCAGTTGAGAGC	<u>36</u>		
123L	F	GTAGATTACACTATGGATATGG	<u>37</u>	60	SCAR (a,b)
	R	CAGTTAGCAGCAATGTCAGC	<u>38</u>		
123L2	F	CATTCAACTAGGCCAAAAGTGG	<u>39</u>	59	SCAR (a,b); DraI (c)
	R	CCAGGTAGGTGTTTCTTCC	<u>40</u>		
123R	F	GTTCTAAGTCAGATGCCACC	<u>41</u>	62	SCAR (a,b)
	R	AAGTGCTCCAACACGAGCC	<u>42</u>		

133R	F	TGAGTTCTCTTACCCTGCG	<u>43</u>	60	SCAR (a,b)
	R	GGATATCCAGCATCAATGCC	<u>44</u>		
133R2	F	GGTGAGCCTCCTTGCATTCC	<u>45</u>	60	SCAR (a,b)
	R	CCTGAGGGAAGATGTCACG	<u>46</u>		
99L	F	CCTAGTTTAGAGTGAGTAGAC	<u>47</u>	58	SCAR (a,b)
	R	GTGATATATTGCTCAAGGATCC	<u>48</u>		
113R	F	GTTGCTGGCTGTCACTGATC	<u>49</u>	59	SCAR (a,b)
	R	GTGATGTGCAGGGTTCAAGG	<u>50</u>		
67L	F	GATTAGTGTAGATCTTAGCTTG	<u>51</u>	62	MboI (a,b)
	R	AAATCTCTCTCACAATTATCCC	<u>52</u>		
112L	F	CTATTGACTGAACCTGCTGAG	<u>53</u>	56	HaeIII (a); HinfI (c)
	R	TGAAGTCATTTAGTCCACAGC	<u>54</u>		
CT216 (RFLP)	F	AGATCGGAGTGTGAACATGG	<u>55</u>	56	
	R	CTTCTACTTCTAGTCGACTGC	<u>56</u>		
CT216	F	CGTAGTCCATCTGAAGCTCC	<u>57</u>	65	SCAR (a,b)
	R	TCTTCTTCTGCTAGTCGTCG	<u>58</u>		
CT119	F	ACTATTCTCACGTAAGGGGACAC	<u>59</u>	60	HindIII (a,b)
	R	GTGTACATGTATGAACTCTAGC	<u>60</u>		
CT119N	F	GTTCTTTCAATCAGAAAGTAG	<u>61</u>	55	SCAR (a)
	R	CTTTGGATGAGTCAAAAGGCT	<u>62</u>		
14L24L	F	univ14L		60	CfoI (c)
	R	univ24L			
SPB30L	F	CAAGTTACGGCAACCAAGAG	<u>63</u>	57	HpaII (c)
	R	CTTTGACACAGTGTTAGAATGC	<u>64</u>		
SPB39L	F	CGTGATCTAGGAGTTACGAC	<u>65</u>	52	SCAR (c)
	R	CTTATTTTAAATACAAGACATCTGG	<u>66</u>		
24L9spec	F	univ. 14L		56	HhaI (c)
	R	CAGAGGAAAGTCAACCAACG	<u>67</u>		
24Lspec	F	univ. 14L		60	CfoI (c)
	R	CAGAGGAAAGTCAACCAACG	<u>68</u>		
NptII	F	TCGGCTATGACTGGGCACAACAGA	<u>69</u>	70	
	R	AAGAAGGCGATAGAAGGCGATGCG	<u>70</u>		
M13	F	TGTAACACGACGGCCAGT	<u>71</u>	55	
	R	GGAAACAGCTATGACCATG	<u>72</u>		

<sup>1)</sup> Ori: Orientation of the primer; F: forward primer; R: reverse primers

<sup>2)</sup> a: ARG95-3, b: ARP96-11, c: B6a

In the specification at page 74, please replace Table 3B with the following amended Table 3B:

**Table 3B. Overview of primers used for mapping Rpi-blb2**

primer	Ori	Sequence <sup>1)</sup>	SEQ ID NO:
ARO 73	F	TTCAGCACAAATACCAAT	<u>73</u>
ARO 74	R	GATGTTCCCCTTCTTTTA	<u>74</u>
ARO 77	R	TTGTGGTTATCGATGAGAAT	<u>75</u>
ARO 79	R	ACCTGGCGTTCCTTATTTTT	<u>76</u>
ARO 94		NGTCASWGANAWGAA	<u>77</u>
ARO 128	F	GATGGAGCGGAAAAGCCGGTG	<u>78</u>
ARO 129	F	GGTGTTTTGTAGCATCTCCAG	<u>79</u>
ARO 295		CCATGATTACGCCAAGCTGG	<u>80</u>
ARO 296		GGTTTTCCCAGTCACGACGT	<u>81</u>
univ14L	F	AGAAAGCTCACCAGTGGACC	<u>82</u>
univ24L	R	ATTTATGGCTGCAGAGGACC	<u>83</u>
123Mi	R	AAGTCCAATTGCTCATCCATC	<u>84</u>
14L2	R	TGCACCATGCACGAAGGTC	<u>85</u>
24L2	F	CAATWTTGGTCCCGAAATTGG	<u>86</u>
ARF1F	F	ATGGAAAAACGAAAAGATAATGAAG	<u>87</u>
ARF1R	R	CTACTTAAATAACGGGATATCCTTC	<u>88</u>
ARO 602	F	CCCATGACTCCTTGAGTTTG	<u>89</u>
S1		GGTGGGGTTGGGAAGACAACG	<u>90</u>
EcoR1+0		GTAGACTGCGTACCAATTC	<u>91</u>
MseI+0		GATGAGTCCTGAGTAA	<u>92</u>
ARO 769		GTGCTTCATTCAAACCTCAAGGAG	<u>95</u>
ARO 770		CTGAAGTAGAAAACTCACTGTAGA	<u>96</u>
ARO 771		GTTTGAAAAGATTGCAATTGCATG	<u>97</u>
ARO 772		CTCAGCCATCAGTTGAAACAGAGA	<u>98</u>
ARO 774		GAGAGAGATTCAAGAGGAGGAAGC	<u>99</u>

<sup>1)</sup> N=A+T+G+C, S=G+C, W=A+T

In the specification at page 79 line 21, please replace the paragraph starting with “Figure 13” with the following amended paragraph:

**Figure 13.** Nucleic acid sequences coding for the Rpi-blb2 gene. A. Coding nucleic acid sequence of the Rpi-blb2 gene (SEQ ID NO: 1). B. Coding nucleic acid sequence of the Rpi-blb2 gene including the intron sequence (position 43-128) (SEQ ID NO: 3). C. Sequence of the 7967 bp Sau3AI genomic DNA fragment of ARD 1197-16 BAC 211 present in p211F-C12 (SEQ ID NO: 5), one of the two the genetic constructs used for genetic complementation for late blight

resistance. The genomic fragment harbours the Rpi-blb2 gene including natural regulatory elements necessary for correct expression of the gene. The initiation codon (ATG position 1546-1548) and the termination codon (TAG position 5433-5435) are underlined. **D.** Sequence of the 9949 bp Sau3AI genomic DNA fragment of *S. bulbocastanum* 2002 BAC BlbSP39 present in pSP39-20 (SEQ ID NO: 6), one of the two the genetic constructs used for genetic complementation for late blight resistance. The genomic fragment harbours the Rpi-blb2 gene including natural regulatory elements necessary for correct expression of the gene. The initiation codon (ATG position 1413-1415) and the termination codon (TAG position 5300-5303) are underlined.

In the specification at page 79 line 36, please replace the paragraph starting with “Figure 14” with the following amended paragraph:

**Figure 14.** Putative Rpi-blb2 gene structure and deduced Rpi-blb2 protein sequence. **A.** Schematic representation of the Rpi-blb2 gene structure. Horizontal lines indicate exons. Open boxes represent coding sequence. Lines angled downwards indicate the positions of intron sequences. **B.** Deduced Rpi-blb2 protein sequence (SEQ ID NO: 4). The amino acid sequence deduced from the DNA sequence of Rpi-blb2 is divided into three domains (LZ, NBS and LRR). Hydrophobic residues in domain A that form the first residue of heptad repeats of the potential leucine zipper (LZ) domain are underlined. Conserved motifs in R proteins are written in lowercase and in italic in the NBS domain. Residues matching the consensus of the cytoplasmic LRR are indicated in bold in the LRR domain. Dots in the sequence have been introduced to align the sequence to the consensus LRR sequence of cytoplasmic LRRs.

In the specification at page 80 line 8, please replace the paragraph starting with “Figure 15” with the following amended paragraph:

**Figure 15.** Alignment of the deduced protein products encoded by Rpi-blb2 (SEQ ID NO: 4), Mi-1.1 (SEQ ID NO: 8) and Mi-1.2 (SEQ ID NO: 10). The complete amino acid sequence of Rpi-blb2 is shown and amino acid residues from Mi-1.1 and Mi-1.2 that differ from the corresponding residue in Rpi-blb2. Dashes indicate gaps inserted to maintain optimal alignment. Amino acid residues that are specific for Rpi-blb2, when compared to those at corresponding

positions in Mi-1.1 and Mi-1.2 are highlighted in bold and red. The regions of the LRRs that correspond to the  $\beta$ -strand/ $\beta$ -turn motif xxLxLxxxx are underlined. Conserved motifs in the NBS domain are indicated in lowercase. A vertical line indicates the division between CC-NBS and LRR region. The position of the VLDL motif which is conserved in the third LRR of many plant R proteins but not in Rpi-blb2 is indicated by a shaded rectangle.

In the specification at page 80 line 19, please replace the paragraph starting with “Figure 16” with the following amended paragraph:

**Figure 16.** CLUSTAL W (1.82) Multiple Sequence Alignments of Mi1.1 (SEQ ID NO: 7), Mi1.2 (SEQ ID NO: 9) and Rpi-blb2 (SEQ ID NO: 1) nucleic acids.

In the specification at page 80 line 22, please replace the paragraph starting with “Figure 17” with the following amended paragraph:

**Figure 17.** CLUSTAL W (1.82) Multiple Sequence Alignments of Mi1.1 (SEQ ID NO: 8), Mi1.2 (SEQ ID NO: 10) and Rpi-blb2 (SEQ ID NO: 2) proteins.